#4 ~~12E12~~
6/12/01

LAW OFFICES

McDonnell Boehnen Hulbert & Berghoff

MBHB

Donald L. Zuhn, Ph.D.
Direct Dial: (312) 913-2132
E-Mail: zuhn@mbhb.com

32ᴺᴰ Floor
300 South Wacker Drive
Chicago, Illinois 60606
Telephone: (312) 913-0001
Facsimile: (312) 913-0002

TO:	**Examiner Brian Whiteman**	FROM:	Donald Zuhn
COMPANY:	PTO Fax Center Crystal Mall 1; Group 1633	DATE:	June 4, 2001
FAX NUMBER:	703-305-7401	FIRM CODE:	349-118
PHONE NUMBER:		NO. OF PAGES:	9 (including cover page)

Re: Restriction Election Facsimile Transmission
U.S. Patent Application No. 09/729,264, filed November 28, 2000
"B7-Like Molecules and Uses Thereof"
Welcher *et al.*

60214512

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
(Case No. 01,668)

PATENT

In re Application of: Welcher et al.   )
)
Serial No.:   09/729,264   ·   )   Before the Examiner: B. Whiteman
)
Filed: November 28, 2000   )   Group Art Unit: 1633
)
For: B7-Like Molecules and Uses   )
       Thereof   )

Commissioner for Patents
Washington, D.C. 20231

Sir:

TRANSMITTAL LETTER

In regard to the above identified application:

1.   We are transmitting herewith the attached

    Response to Restriction Requirement

2.   Please charge any additional fees to Deposit Account No. 13-2490.

3.   The undersigned hereby certifies that this Transmittal Letter and this paper, as described in paragraph 1 herein above, are being facsimile transmitted to the Patent and Trademark Office (PTO Fax Center in Crystal Mall 1; Fax No. 703-305-7401) on June 4, 2001.

                                Respectfully submitted,
                                McDonnell Boehnen Hulbert & Berghoff

Dated: June 4, 2001   By: _____
                                       Donald Zuhn, Ph.D
                                       Reg. No. P-48,710

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
(Case No. 01,668)

PATENT

In re Application of: Welcher et al.   )
)
Serial No.:   09/729,264   )   Before the Examiner: B. Whiteman
)
Filed: November 28, 2000   )   Group Art Unit: 1633
)
For: B7-Like Molecules and Uses   )
       Thereof   )

Commissioner for Patents
Washington, D.C. 20231

Sir:

RESPONSE TO RESTRICTION REQUIREMENT
MAILED MAY 4, 2001

Responsive to the Restriction Requirement, mailed May 4, 2001, Applicants elect to prosecute claims 1-8, 10, 11, 46-48, and 55, designated as Group I by the Examiner. Applicants further elect to prosecute the species of the nucleic acid sequence as set forth in SEQ ID NO: 1, with traverse. The basis for Applicants' traversal of the requirement is as follows.

Applicants respectfully submit that there will be no undue hardship on the Office in performing a search with respect to the nucleic acid sequences of SEQ ID NOs: 1, 3, and 5. The putative secreted portion of the human B7-Like polypeptides encoded by these sequences (i.e., amino acid residues 9-382 of the amino acid sequence encoded by the nucleic acid sequence of SEQ ID NO: 1 and amino acid residues 13-386 of the amino acid sequences encoded by the nucleic acid sequences of SEQ ID NOs: 3 and 5) share a sequence identity of greater than 99% (Exhibit A). The open reading frames for each of these sequences share a sequence identity of greater than 97% (Exhibit B). Sequence alignments were performed using the application MacVector 7.0 (Accelrys, Cambridge, UK; http://www.accelrys.com) at the default settings.

Applicants do not believe any additional fee is required. However, the Commissioner is authorized to charge any deficiency to Deposit Account No. 13-2490. If Examiner Whiteman

believes it to be helpful, he is invited to contact the undersigned attorney by telephone at (312) 913-0001.

Respectfully submitted,
McDonnell Boehnen Hulbert & Berghoff

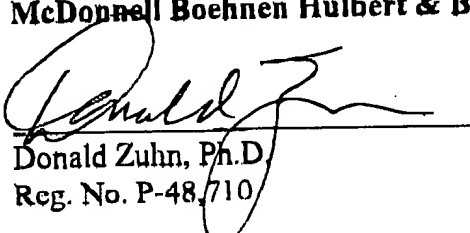Dated: June 4, 2001

By: _____

Donald Zuhn, Ph.D.
Reg. No. P-48,710

EXHIBIT A

ClustalW (v1.4) multiple sequence alignment

3 Sequences Aligned   Alignment Score = 7182
Gaps Inserted = 0   Conserved Identities = 371

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: blosum

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: blosum

Processing time: 0.9 seconds


```
SEQ05_AA    1 MERHLLTVPEAVGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITND  70
SEQ03_AA    1 MVAGAMENRDPPGSGSGNEVIEGPQNARVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITND  70
SEQ01_AA    1      MGLVIFLHGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITND  66
                     ***********  ******************************************************

SEQ05_AA   71 RFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVVAENEPCEV 140
SEQ03_AA   71 RFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVVAENEPCEV 140
SEQ01_AA   67 RFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVVAENEPCEV 136
                *********************************************************************

SEQ05_AA  141 TCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVN 210
SEQ03_AA  141 TCLPSHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVN 210
SEQ01_AA  137 TCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVN 206
                ********  ***********************************************************

SEQ05_AA  211 LTVIRCPQDTGGGINIPGVLSSLPSLGPSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCC 280
SEQ03_AA  211 LTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCC 280
SEQ01_AA  207 LTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCC 276
                ********************************************************************

SEQ05_AA  281 RCCFCCRRKRGFRIQFQKKSEKEKTNKETETESGNENSGYNSDEQKTTETASLPPKSCESSDPEQRNSSC 350
SEQ03_AA  281 RCCFCCRRKRGFRIQFQKKSEKEKTNKETETESGNENSGVNSDEQKTTDTASLPPKSCESSDPEQRNSSC 350
SEQ01_AA  277 RCCFCCRRKRGFRIQFQKKSEKEKTNKETETESGNENSGYNSDEQKTTDTASLPPKSCESSDPEQRNSSC 346
                *********************************************,**********************

SEQ05_AA  351 GPPHQRADQRPPRPASHPQASFNLASPEKVSNTTVV 386
SEQ03_AA  351 GPPHQRADQRPPRPASHPQASFNLASPEKVSNTTVV 386
SEQ01_AA  347 GPPHQRADQRPPRPASHPQASFNLASPEKVSNTTVV 382
                ************************************
```

EXHIBIT B

Nucleic acid sequence alignment for SEQ ID NO: 1, 3, and 5 open reading frames.

Search Analysis for Sequence: SEQ01_ORF   Matrix: DNA database matrix
Search from 1 to 1146 where origin = 1   Score Region from 1 to 1146
Date: June 4, 2001   Maximum possible score: 4584
Time: 16:32:66

Database: Folder 'untitled folder'

```
              10        20        30        40        50        60        70
SEQ01_ORF    atggggcttgtgattttcctccacggttctgggtctggtaatgaagtcatagaaggcccccagaatgcaa

1. SEQ03_ORF   20        30        40        50        60        70        80
[ 4488 ]     ATGGAAAAT-AGA-GACCCACC-CGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAAAATGCAA>
             ||||    |   ||    || || ||||||||||||||||||||||||||||||||||||||| |||||||
SEQ01_ORF    atggggcttgtgattttcctccacggttctgggtctggtaatgaagtcatagaaggcccccagaatgcaa

2. SEQ05_ORF                       40        50        60        70        80
[ 4486 ]                    CTGTA-GGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAGAATGCAA>
                            || | ||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF                   ctccacggttctgggtctggtaatgaagtcatagaaggcccccagaatgcaa


              80        90       100       110       120       130       140
SEQ01_ORF    cagtcctgaagggctcccaggctcgcttcaactgcaccgtctcccagggctggaagctcatcatgtgggc

1. SEQ03_ORF   90       100       110       120       130       140       150
[ 4488 ]     GAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGC>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    cagtcctgaagggctcccaggctcgcttcaactgcaccgtctcccagggctggaagctcatcatgtgggc

2. SEQ05_ORF   90       100       110       120       130       140       150
[ 4486 ]     CAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGC>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    cagtcctgaagggctcccaggctcgcttcaactgcaccgtctcccagggctggaagctcatcatgtgggc


             150       160       170       180       190       200       210
SEQ01_ORF    tctcagtgacatggtggtgctaagcgtcaggcccatggagcccatcatcaccaatgaccgcttcacctct

1. SEQ03_ORF  160       170       180       190       200       210       220
[ 4488 ]     TCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCTTCACCTCT>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    tctcagtgacatggtggtgctaagcgtcaggcccatggagcccatcatcaccaatgaccgcttcacctct

2. SEQ05_ORF  160       170       180       190       200       210       220
[ 4486 ]     TCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCTTCACCTCT>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    tctcagtgacatggtggtgctaagcgtcaggcccatggagcccatcatcaccaatgaccgcttcacctct


             220       230       240       250       260       270       280
SEQ01_ORF    cagaggtacgaccagggcgggaacttcacctcggagatgatcatccacaatgtggagcccagtgattcgg

1. SEQ03_ORF  230       240       250       260       270       280       290
[ 4488 ]     CAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATGTGGAGCCCAGTGATTCGG>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    cagaggtacgaccagggcgggaacttcacctcggagatgatcatccacaatgtggagcccagtgattcgg

2. SEQ05_ORF  230       240       250       260       270       280       290
[ 4486 ]     CAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATGTGGAGCCCAGTGATTCGG>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    cagaggtacgaccagggcgggaacttcacctcggagatgatcatccacaatgtggagcccagtgattcgg
```

1

```
                    290       300       310       320       330       340       350
SEQ01_ORF   ggaacatcagatgcagcctccagaacagtcgcctgcatggatctgcttaccttaccgtccaagttatggg

1. SEQ03_ORF     300       310       320       330       340       350       360
[ 4488 ]    GGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGTTATGGG>
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF   ggaacatcagatgcagcctccagaacagtcgcctgcatggatctgcttaccttaccgtccaagttatggg

2. SEQ05_ORF     300       310       320       330       340       350       360
[ 4486 ]    GGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGTTATGGG>
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF   ggaacatcagatgcagcctccagaacagtcgcctgcatggatctgcttaccttaccgtccaagttatggg


                    360        370       380       390       400       410       420
SEQ01_ORF   agagctgttcattcccagtgttaatcttgtagtcgctgagaatgaaccttgtgaagttacttgtctaccc

1. SEQ03_ORF     370       380       390       400       410       420       430
[ 4488 ]    AGAGCTGTTCATTCCCAGTGTTAATCTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCC>
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF   agagctgttcattcccagtgttaatcttgtagtcgctgagaatgaaccttgtgaagttacttgtctaccc

2. SEQ05_ORF     370       380       390       400       410       420       430
[ 4486 ]    AGAGCTGTTCATTCCCAGTGTTAATCTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCC>
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF   agagctgttcattcccagtgttaatcttgtagtcgctgagaatgaaccttgtgaagttacttgtctaccc


                    430       440       450       460       470       480       490
SEQ01_ORF   tcacactggacccggctcccggatatttcctgggagctcggtctcctggtcagccattcaagctattatt

1. SEQ03_ORF     440       450       460       470       480       490       500
[ 4488 ]    TCACACTGGACCTGGCTCCCGGATATTTCCTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATT>
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF   tcacactggacccggctcccggatatttcctgggagctcggtctcctggtcagccattcaagctattatt

2. SEQ05_ORF     440       450       460       470       480       490       500
[ 4486 ]    TCACACTGGACCCGGCTCCCGGATATTTCCTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATT>
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF   tcacactggacccggctcccggatatttcctgggagctcggtctcctggtcagccattcaagctattatt


                    500       510       520       530       540       550       560
SEQ01_ORF   ttgttccggagcccagcgaccttcaaagtgcagtgagcatcctggctctgacccacagagcaatgggac

1. SEQ03_ORF     510       520       530       540       550       560       570
[ 4488 ]    TTGTTCCGGAGCCCAGCGACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAATGGGAC>
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF   ttgttccggagcccagcgaccttcaaagtgcagtgagcatcctggctctgacccacagagcaatgggac

2. SEQ05_ORF     510       520       530       540       550       560       570
[ 4486 ]    TTGTTCCGGAGCCCAGCGACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAATGGGAC>
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF   ttgttccggagcccagcgaccttcaaagtgcagtgagcatcctggctctgacccacagagcaatgggac


                    570       580       590       600       610       620       630
SEQ01_ORF   tttgacttgcgtggctacctggaagagcctgaaggcccgcaagtctgcaactgtaaatctcactgtgatt

1. SEQ03_ORF     580       590       600       610       620       630       640
[ 4488 ]    TTTGACTTGCGTGGCTACCTGGAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACTGTGATT>
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF   tttgacttgcgtggctacctggaagagcctgaaggcccgcaagtctgcaactgtaaatctcactgtgatt

2. SEQ05_ORF     580       590       600       610       620       630       640
[ 4486 ]    TTTGACTTGCGTGGCTACCTGGAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACTGTGATT>
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF   tttgacttgcgtggctacctggaagagcctgaaggcccgcaagtctgcaactgtaaatctcactgtgatt
```

```
                          640        650        660        670        680        690        700
SEQ01_ORF    cggtgtccccaagacactggaggtggtattaatattccaggtgtattatcaagtttaccgagtttaggtt

1. SEQ03_ORF          650        660        670        680        690        700        710
[ 4488 ]     CGGTGTCCCCAAGACACTGGAGGTGGTATTAATATTCCAGGTGTATTATCAAGTTTACCGAGTTTAGGTT>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    cggtgtccccaagacactggaggtggtattaatattccaggtgtattatcaagtttaccgagtttaggtt

2. SEQ05_ORF          650        660        670        680        690        700        710
[ 4486 ]     CGGTGTCCCCAAGACACTGGAGGTGGTATTAATATTCCAGGTGTATTATCAAGTTTACCGAGTTTAGGTT>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    cggtgtccccaagacactggaggtggtattaatattccaggtgtattatcaagtttaccgagtttaggtt


                          710        720        730        740        750        760        770
SEQ01_ORF    tttcattgcctacttggggcaaagttggacttggactagcaggcaccatgcttctgacgccgacgtgtac

1. SEQ03_ORF          720        730        740        750        760        770        780
[ 4488 ]     TTTCATTGCCTACTTGGGGCAAAGTTGGACTTGGACTAGCAGGCACCATGCTTCTGACGCCGACGTGTAC>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    tttcattgcctacttggggcaaagttggacttggactagcaggcaccatgcttctgacgccgacgtgtac

2. SEQ05_ORF          720        730        740        750        760        770        780
[ 4486 ]     TTTCATTGCCTACTTGGGGCAAAGTTGGACTTGGACTAGCAGGCACCATGCTTCTGACGCCGACGTGTAC>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    tttcattgcctacttggggcaaagttggacttggactagcaggcaccatgcttctgacgccgacgtgtac


                          780        790        800        810        820        830        840
SEQ01_ORF    tcttacaatacgctgctgctgctgccgccgtcgttgttgtggctgcaactgctgctgccgttgttgtttc

1. SEQ03_ORF          790        800        810        820        830        840        850
[ 4488 ]     TCTTACAATACGCTGCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCCGTTGTTGTTTC>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    tcttacaatacgctgctgctgctgccgccgtcgttgttgtggctgcaactgctgctgccgttgttgtttc

2. SEQ05_ORF          790        800        810        820        830        840        850
[ 4486 ]     TCTTACAATACGCTGCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCCGTTGTTGTTTC>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    tcttacaatacgctgctgctgctgccgccgtcgttgttgtggctgcaactgctgctgccgttgttgtttc


                          850        860        870        880        890        900        910
SEQ01_ORF    tgctgtagaagaaaaagaggatttcgtattcaatttcaaaagaaatctgaaaaagagaagacaaacaaag

1. SEQ03_ORF          860        870        880        890        900        910        920
[ 4488 ]     TGCTGTAGAAGAAAAAGAGGATTTCGTATTCAATTTCAAAAGAAATCTGAAAAAGAGAAGACAAACAAAG>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    tgctgtagaagaaaaagaggatttcgtattcaatttcaaaagaaatctgaaaaagagaagacaaacaaag

2. SEQ05_ORF          860        870        880        890        900        910        920
[ 4486 ]     TGCTGTAGAAGAAAAAGAGGATTTCGTATTCAATTTCAAAAGAAATCTGAAAAAGAGAAGACAAACAAAG>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    tgctgtagaagaaaaagaggatttcgtattcaatttcaaaagaaatctgaaaaagagaagacaaacaaag


                          920        930        940        950        960        970        980
SEQ01_ORF    aaactgagacagaaagtggaaatgaaaactccggctacaattcagatgaacaaaagaccacagacaccgc

1. SEQ03_ORF          930        940        950        960        970        980        990
[ 4488 ]     AAACTGAGACAGAAAGTGGAAATGAAAACTCCGGCTACAATTCAGATCAACAAAACACCACACACACCCC>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    aaactgagacagaaagtggaaatgaaaactccggctacaattcagatgaacaaaagaccacagacaccgc

2. SEQ05_ORF          930        940        950        960        970        980        990
[ 4486 ]     AAACTCACACAGAAAGTGGAAATGAAAACTCCGGCTACAATTCAGATGAACAAAAGACCCACAGAAACCCC-
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
SEQ01_ORF    aaactgagacagaaagtggaaatgaaaactccggctacaattcagatgaacaaaagaccacagacaccgc
```

```
                   990       1000      1010      1020      1030      1040      1050
SEQ01_ORF    ttctctccctcccaaatcctgtgaatccagtgatcctgaacaaagaaacagtagctgtggccctcctcac

                   1000      1010      1020      1030      1040      1050      1060
1. SEQ03_ORF
[ 4488 ]     TTCTCTCCCTCCCAAATCCTGTGAATCCAGTGATCCTGAACAAAGAAACAGTAGCTGTGGCCCTCCTCAC>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    ttctctccctcccaaatcctgtgaatccagtgatcctgaacaaagaaacagtagctgtggccctcctcac

                   1000      1010      1020      1030      1040      1050      1060
2. SEQ05_ORF
[ 4486 ]     TTCTCTCCCTCCCAAATCCTGTGAATCCAGTGATCCTGAACAAAGAAACAGTAGCTGTGGCCCTCCTCAC>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    ttctctccctcccaaatcctgtgaatccagtgatcctgaacaaagaaacagtagctgtggccctcctcac


                   1060      1070      1080      1090      1100      1110      1120
SEQ01_ORF    cagcgggctgatcaacgtccacccaggccagcaagtcatccacaggcttcttttaatctggccagtcctg

                   1070      1080      1090      1100      1110      1120      1130
1. SEQ03_ORF
[ 4488 ]     CAGCGGGCTGATCAACGTCCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTTAATCTGGCCAGTCCTG>
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    cagcgggctgatcaacgtccacccaggccagcaagtcatccacaggcttcttttaatctggccagtcctg

                   1070      1080      1090      1100      1110      1120      1130
2. SEQ05_ORF
[ 4486 ]     CAGCGGGCTGATCAACGTCCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTTAATCTGGCCAGTCCTG>
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    cagcgggctgatcaacgtccacccaggccagcaagtcatccacaggcttcttttaatctggccagtcctg


                   1130      1140
SEQ01_ORF    agaaggtcagtaatacaactgtagta

                   1140      1150
1. SEQ03_ORF
[ 4488 ]     AGAAGGTCAGTAATACAACTGTAGTA>
             ||||||||||||||||||||||||||
SEQ01_ORF    agaaggtcagtaatacaactgtagta

                   1140      1150
2. SEQ05_ORF
[ 4486 ]     AGAAGGTCAGTAATACAACTGTAGTA>
             ||||||||||||||||||||||||||
SEQ01_ORF    agaaggtcagtaatacaactgtagta
```

4